



## **Diversity of Lactic acid bacteria isolated from fura produced in Ghana**

Owusu-Kwarteng, James; Tano-Debrah, K.; Glover, R.; Akabanda, F.; Nielsen, Dennis Sandris; Jespersen, Lene

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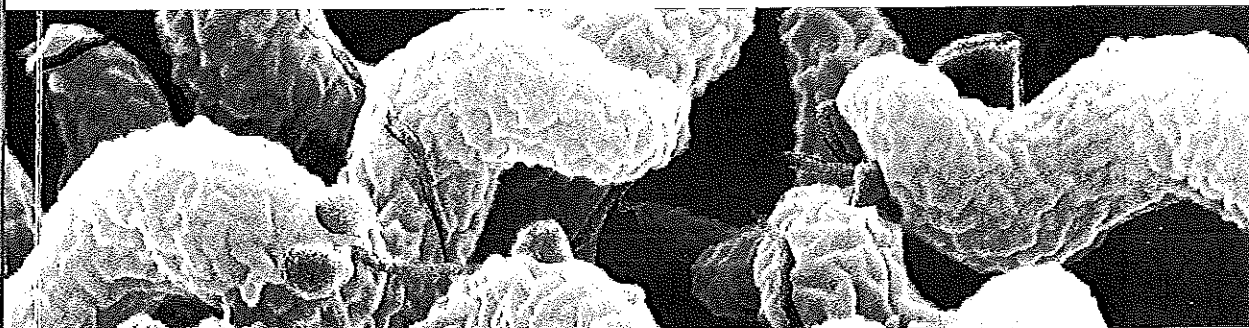
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Hinenoya A	PEC1.77	Ingmer H	PEB1.21		PED2.04	Kanno S
Hinrichs J	PEA1.16		PEB1.23	Javier Y	PED2.01	Kantikova M
Hiraga Chidchom	PED2.11		PEC1.62	Jensen AN	PED1.33	Kapetanakou A
Hocking A	PEB2.56		PEC1.68	Jensen Annette N	PED1.23	
Højberg Ole	PEB1.30		PEB2.21	Jensen BB	PEE2.22	Kapetanakou, Ana:
Holck A.	PEB2.52		PED2.16	Jensen LB	PEB2.45	Karamad Dina
Holvoet, K	PSD1.01	Iñiguez C	PED1.05	Jensen, Annette Nygaard	PSE1.02	Karbancıglu-Güler
Holzapfel W	PEE2.21		PED2.09	Jeong A-R	PED1.34	Karbancıglu-Güle
Holzapfel Wilhelm	PEE2.20	Inoue H	PEC1.77	Jeršek B	PED2.52	Karbassi A
Hondrodinou O	PED2.28	Irkin Reyhan	PED2.60	* Jespersen L	PEA1.36	Karlsen H
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	PEC1.08	Irlinger F	PEA2.04		PEA1.40	Karpiskova R
	PEC1.11	Irmeler Stefan	PEA1.19		PEA1.41	
	PEC1.57	Irmeler, S	PSA1.03		PEB1.32	
	PEC2.01	Isaks A	PED2.13		PEE2.15	Kashi Y
	PEC2.06	Islam Mohammad	PEA1.77		PEE2.24	Kashi Yechezkel
	PED1.03	Ivanova Iskra	PEA2.17	Jespersen Lene	PEA1.10	
	PSC1.06, PSC1.04	Jacobsen T	PEC1.66	Jespersen, L	PSD1.03	Kasimoglu Dogru A
Hoornstra D	PEA1.72		PEC1.67	Ji Y	PEE2.21	Katz T
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Hoshino K	PEE2.13		PEC2.18	Jo MJ	PED1.34	Keller D
Houard E	PED1.08		PEC2.33	Jofré Anna	PEB2.40	Kentish S
Houard E	PED1.22		PEC2.34	Johannessen Gro Skøien	PEC1.56	Khamisse Elissa
Houf, K	PSC1.05		PED1.24	Johannessen GS	PEC1.86	Khan Nazer AH
Houndenoukon M	PEA1.42	Jacxsens Liesbeth	PEC2.35	Johansson T	PEB1.26	Khen B
Houngouigan J	PEA1.38		PEC2.36	Jongorius-Gortemaker BGM	PEB1.06	
	PEA1.42	Jacxsens, L	PSD1.01	Jonkman J	PEA1.55	Killer J
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	PEA1.55	Jaime I	PEC1.54	Jooste P	PEB2.16	KIM H-n
Hovda Maria Befring	PEC1.63		PEC2.20	Jordan K	PEC2.06	Kim H-n
Hradecka Helena	PEE2.12		PEC2.21	Joris Maria-Adelheid	PED1.29	Kim H-Y
Hrušková V	PEB1.20		PEC2.26		PED1.37	Kim Hyun Jung
Huang Yanyan	PEB2.36		PED2.22	Josefsen M	PEC2.01	Kim Y
Huang, Q	PSA2.06		PED2.32	Josefsen Mathilde	PEC1.11	Kim YG
Huber Ingrid	PEE2.11		PED2.43		PSC1.06,	Kim Y-G
Hudecova A	PEC1.04		PED2.44	Juliana Cunha, A	PSA1.04	Kim Yungyeong
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Hultman J	PEA2.28		PEA1.42	Kabisch Jan	PEA2.12	Kjeldgaard Jette
Humblot C	PEA1.44		PEA1.70	Kaesbohrer A	PED2.05	Klanénik A
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Hwang I	PEC1.38		PED2.50	Kahraman O	PEA1.47	
Hwang IG	PEC1.42		PEE2.14	Kakouri A	PEA1.52	
Hyeon J	PEC1.38		PSA1.01	Kalamaki M	PEA1.60	Klinder Annett
Hyeon Ji-Yeon	PEC1.39	Jaloustre Séverine	PEC1.50	Kallipolititis BH	PEB2.33	Klinder, A
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Højberg O	PEE2.22	Janssens K	PEC1.47	Kamata Yoichi	PEB1.13	Kneifel W
Ignatova T	PEA2.17	Jaros D	PEA2.32	Kampmann Y	PEC1.26	Knockaert D
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Iliev M	PEC1.91		PEC1.41	Kang Min-Su	PEB2.10	Knöchel S
Iliopoulos V	PEA2.19	Jasson V	PEC2.15	Kankare M	PEB1.26	
in 't Veld Paul	PEB1.26	Javanmard Majid	PEA2.01	Kan-King-Yu, D	PSC1.01	Kocevski D

PEA1.35 Designing safe probiotic fermented sausages

Margarita Garriga (1), S Bover-Cid (1), R Rubio (1), B Martín (1), T Aymerich (1)  
(1) IRTA, Spain

Within the trends of consumer demands of safe and healthy products, the purpose of the present study was to assess the compatibility between the probiotic strain *Lactobacillus plantarum* 299V and the bioprotective starter culture *Lactobacillus sakei* CTC494 in Spanish fermented sausages. Three independent batches were elaborated: lot 1 (inoculated with *L. plantarum* 299V at  $1.0 \times 10^7$  cfu/g), lot 2 (*L. sakei* CTC494 at  $3.0 \times 10^8$  cfu/g) and lot 3 (with both strains). Technological parameters and microbial counts were evaluated during fermentation and ripening of sausages. Randomly amplified polymorphic DNA (RAPD)-PCR was used to monitor the competitiveness of the probiotic and the bioprotective starter cultures. LAB counts achieved  $10^9$  cfu/g in all batches and RAPD-PCR profiles obtained at each sampling time confirmed the implantation of the assayed strains. Nevertheless, in the compatibility lot 3, *L. sakei* CTC 494 was able to grow until  $10^8$  cfu/g, while *L. plantarum* 299V survived keeping counts at  $10^7$  cfu/g until the end of ripening. This work proved the feasibility to combine probiotic and bioprotective culture strains in fermented sausages.

\* PEA1.36 Diversity of Lactic acid bacteria isolated from fura produced in Ghana

James Owusu-Kwarteng (1), K Tano-Debrah (2), R Glover (1), F Akabanda (1), D S. Nielsen (3), L Jespersen (3)  
(1) University for Development Studies, Navrongo, Ghana  
(2) University of Ghana, Legon  
(3) University of Copenhagen, Faculty of Life Science, Denmark

The majority of traditional cereal-based foods consumed in Africa are processed by spontaneous fermentation and are important as weaning foods for infants and as dietary staples for adults. *Fura*, is a popular millet-based dumpling consumed throughout West Africa, particularly Nigeria, Burkina-Faso and Ghana. The biodiversity of lactic acid bacteria isolated during the processing of millet into *fura*, was investigated in a range of production units in northern Ghana. A total of 181 strains of lactic acid bacteria were isolated. Lactic acid bacteria biodiversity was evaluated by both phenotypic and molecular based methods. Molecular biology-based grouping of strains was performed using rep-PCR (GTG<sub>5</sub>-primer) followed by 1.5% agarose gel electrophoresis. Based on the phenotypic and genotypic grouping, representative isolates were selected and the 16S rRNA gene sequenced. Based on the molecular analyses it was concluded that production of *fura* in the Northern part of Ghana is dominated by *Lactobacillus fermentum*, *Lactobacillus plantarum*, *Lactobacillus pentosus*, *Lactobacillus reuteri*, *Lactobacillus salivarius*, *Pediococcus acidilactici*, *Pediococcus pentosaceus*, *Weissella confusa* and *Weissella cibaria*. One group of strains with similar characteristics could not be identified based on the methods used and needs to be investigated in further details in order to define its species assignation or the possibility of being a new so far undefined species. The development of starter culture from the dominating organisms is important for the potential production of standardized *fura* at a commercial, small industrial scale, and for the improvement of its acceptability, microbiological stability and hygienic safety.